

SEQUENCE LISTING

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 Steele, Doug
 Jones, Robert M.

<120> Tau-Conotoxin Peptides

<130> Tau-Conopeptides

<140>
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<150> US 60/118,642
 <151> 1999-02-04

<160> 49

<170> PatentIn Ver. 2.0

<210> 1
 <211> 23
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Generic
 Sequence for Tau Conopeptides

<220>
 <221> PEPTIDE
 <222> (1)..(2)
 <223> Xaa at residue 1 is Asp, Glu or gamma-carboxy-Glu
 (Gla); Xaa at residue 2 is des-Xaa, Gln, Asn, Glu,
 Trp (D or L), neo-Trp, halo-Trp, any unnatural
 aromatic amino acid.

<220>
 <221> PEPTIDE
 <222> (3)..(4)
 <223> Xaa at residue 3 is des-Xaa, Gly, Ala, Asn or Gln;
 Xaa at residue 4 is des-Xaa4,Val, Leu (D or L),
 Ile, Ala, Gly, Glu, Gla, Asp, Ser, Thr, Phe, Trp
 (D or L), neo-Trp, halo-Trp (D or L) or any

<220>
 <221> PEPTIDE
 <222> (4)..(7)
 <223> unnatural aromatic amino acid; Xaa at residue 7 is
 Pro, hydroxy-Pro, Gln, Asn, Glu, Gla, Ala, Gly,
 Lys, Arg, Ile, Val, homoarginine, ornithine,
 N-methyl-Lys, N,N-dimethyl-Lys,
 N,N,N-trimethyl-Lys or

<220>
 <221> PEPTIDE
 <222> (7)..(8)
 <223> any unnatural basic amino acid; Xaa at residue 8
 is Val, Phe, Thr, Ser, Glu, Gla, Asp, Asn, Gln,
 Ala, Gly, Ile, Leu (D or L), Met, Pro,

hydroxy-Pro, Arg, homoarginine, ornithine, Lys,
N-methyl-Lys,

<220>

<221> PEPTIDE

<222> (8)..(9)

<223> N,N,-dimethyl-Lys, N,N,N-trimethyl-Lys, any
unnatural basic amino acid or any unnatural
aromatic amino acid; Xaa at residue 9 is Val, Ile,
Asn, Leu (D or L), Gln, Gly, Ala, Phe, Glu, Gla,
Arg,

<220>

<221> PEPTIDE

<222> (9)..(10)

<223> ornithine, arginine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any
unnatural basic amino acid or any unnatural
aromatic amino acid; Xaa at residue 10 is Ile, Leu
(D or L), Met, Thr,

<220>

<221> PEPTIDE

<222> (10)

<223> Ser, Pro, hydroxy-Pro, Gln, Asp, Glu, Gla, Asn,
Arg, homoarginine, ornithine, Lys, N-methyl-Lys,
N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, Tyr,
nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,

<220>

<221> PEPTIDE

<222> (10)..(11)

<223> O-phospho-Tyr, nitro-Tyr, any unnatural basic
amino acid, any unnatural aromatic amino acid or
any unnatural hydroxy containing amino acid; Xaa
at residue 11 is des-Xaa, Ala, Gly, Asp, Glu, Gla,

<220>

<221> PEPTIDE

<222> (11)

<223> Trp (D or L), neo-Trp, halo-Trp (D or L), Lys,
N-methyl-Lys, N,N-dimethyl-Lys,
N,N,N-trimethyl-Lys, Arg, homoarginine, ornithine,
Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr,
O-sulpho-Tyr, O-phospho-Tyr,

<220>

<221> PEPTIDE

<222> (11)..(14)

<223> nitro-Tyr or any unnatural basic amino acid; Xaa
at residue 14 is des-Xaa, Ile, Leu (D or L), Val,
Glu, Gla, Asp, Thr, Ser, Pro, hydroxy-Pro, Trp (D
or L), neo-Trp, halo-Trp (D or L), Phe, any

<220>

<221> PEPTIDE

<222> (14)..(15)

<223> unnatural aromatic amino acid or any unnatural
hydroxy containing amino acid; Xaa at residue 15
is des-Xaa11, Gln, Asn, Leu (D or L), Ile, Val,
Ala, Gly, Trp (D or L), neo-Trp, halo-Trp (D or
L), Arg,

<220>

<221> PEPTIDE
 <222> (15)..(16)
 <223> homoarginine, ornithine, Lys, N-methy-Lys,
 N,N-dimethyl-Lys, N,N,N-trimethyl-Lys, any
 unnatural basic amino acid or any unnatural
 aromatic amino acid; Xaa at residue 16 is des-Xaa,
 Ala, Gly, Phe,

<220>
 <221> PEPTIDE
 <222> (16)..(17)
 <223> Trp (D or L), neo-Trp, halo-Trp (D or L) or any
 unnatural aromatic amino acid; Xaa at residue 17
 is des-Xaa, Glu, Gla, Asp, Phe or any unnatural
 aromatic amino acid.

<220>
 <221> PEPTIDE
 <222> (18)..(19)
 <223> Xaa at residue 18 is des-Xaa, Ile, Val or Leu (D
 or L); Xaa at residue 19 is des-Xaa, Thr, Ser,
 Arg, homoarginine, ornithine, Lys, N-methy-Lys,
 N,N-dimethyl-Lys, N,N,N-trimethyl-Lys or any
 unnatural

<220>
 <221> PEPTIDE
 <222> (19)..(22)
 <223> basic amino acid; Xaa at residue 20 is des-Xaa,
 Glu, Gla or Asp; Xaa at residue 21 is des-Xaa, Asn
 or Gln; Xaa at residue 22 is des-Xaa, Asp, Glu or
 Gla.

<220>
 <221> PEPTIDE
 <222> (23)
 <223> Xaa at residue 23 is des-Xaa, Phe or any unnatural
 aromatic amino acid.

<400> 1
 Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20

<210> 2
 <211> 11
 <212> PRT
 <213> Conus aulicus

<220>
 <221> PEPTIDE
 <222> (4)..(8)
 <223> Xaa at residue 4 is Pro or hydroxy-Pro; Xaa at
 residue 8 is Tyr, nor-Tyr, mono-halo-Tyr,
 di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or
 nitro-Tyr.

<220>
 <221> PEPTIDE
 <222> (11)
 <223> Xaa at residue 11 is Trp (D or L), neo-Trp or

halo-Trp (D or L).

<400> 2

Phe Cys Cys Xaa Val Ile Arg Xaa Cys Cys Xaa
1 5 10

<210> 3

<211> 11

<212> PRT

<213> Conus aulicus

<220>

<221> PEPTIDE

<222> (4)..(8)

<223> Xaa at residue 4 is Pro or hydroxy-Pro; Xaa at residue 8 is Tyr, nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr.

<220>

<221> PEPTIDE

<222> (11)

<223> Xaa at residue 11 is Trp (D or L), neo-Trp or halo-Trp (D or L).

<400> 3

Phe Cys Cys Xaa Phe Ile Arg Xaa Cys Cys Xaa
1 5 10

<210> 4

<211> 10

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (6)..(7)

<223> Xaa at residue 6 is Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr or nitro-Tyr; Xaa at residue 7 is Trp (D or L), neo-Trp or halo-Trp (D or L).

<400> 4

Cys Cys Gln Thr Phe Xaa Xaa Cys Cys Gln
1 5 10

<210> 5

<211> 13

<212> PRT

<213> Conus geographus

<220>

<221> PEPTIDE

<222> (1)..(3)

<223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at residue 3 is Trp (D or L), neo-Trp or halo-Trp (D or L); Xaa at residue 6 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<220>

<221> PEPTIDE

<222> (7)
 <223> Xaa at residue 7 is Glu or gamma-carboxy-Glu.

<400> 5
 Xaa Gly Xaa Cys Cys Xaa Xaa Asn Ile Ala Cys Cys Ile
 1 5 10

<210> 6
 <211> 10
 <212> PRT
 <213> Conus quercinus

<400> 6
 Gly Cys Cys Ala Arg Leu Thr Cys Cys Val
 1 5 10

<210> 7
 <211> 12
 <212> PRT
 <213> Conus purpurascens

<220>
 <221> PEPTIDE
 <222> (5)..(6)
 <223> Xaa at residue 5 is Pro or hydroxy-Pro; Xaa at
 residue 6 is Lys, N-methyl-Lys, N,N-dimethyl-Lys
 or N,N,N-trimethyl-Lys.

<400> 7
 Asn Gly Cys Cys Xaa Lys Gln Met Arg Cys Cys Thr
 1 5 10

<210> 8
 <211> 15
 <212> PRT
 <213> Conus imperialis

<220>
 <221> PEPTIDE
 <222> (2)..(15)
 <223> Xaa at residues 2 and 15 is Trp (D or L), neo-Trp
 or halo-Trp (D or L); Xaa at residue 8 is Lys,
 N-methyl-Lys, N,N-dimethyl-Lys or
 N,N,N-trimethyl-Lys; Xaa at residues 10 and 14 is
 Pro or hydroxy-Pro.

<400> 8
 Asp Xaa Asn Ser Cys Cys Gly Xaa Asn Xaa Gly Cys Cys Xaa Xaa
 1 5 10 15

<210> 9
 <211> 13
 <212> PRT
 <213> Conus geographus

<220>
 <221> PEPTIDE
 <222> (1)..(6)
 <223> Xaa at residue 1 is Gln or pyro-Glu; Xaa at
 residue 2 is Trp (D or L), neo-Trp or halo-Trp (D

or L); Xaa at residue 6 is Lys, N-methyl-Lys, N,N,-dimethyl-Lys or N,N,N-trimethyl-Lys.

<220>

<221> PEPTIDE

<222> (7)

<223> Xaa at residue 7 is Glu or gamma-carboxy-Glu.

<400> 9

Xaa Gly Xaa Cys Cys Xaa Xaa Asn Ile Arg Cys Cys Val
1 5 10

<210> 10

<211> 15

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1 and 4 is Glu or gamma-carboxy-Glu; Xaa at residue 7 is Trp (D or L), neo-Trp or halo-Trp (D or L); Xaa at residue 13 is Pro or hydroxy-Pro.

<400> 10

Xaa Cys Cys Xaa Asp Gly Xaa Cys Cys Thr Ala Ala Xaa Leu Thr
1 5 10 15

<210> 11

<211> 15

<212> PRT

<213> Conus textile

<220>

<221> PEPTIDE

<222> (4)..(13)

<223> ; Xaa at residue 4 is Glu or gamma-carboxy-Glu; Xaa at residue 7 is Trp (D or L) neo-Trp or halo-Trp (D or L); Xaa at residue 13 is Pro or hydroxy-Pro.

<400> 11

Gly Cys Cys Xaa Asp Gly Xaa Cys Cys Thr Ala Ala Xaa Leu Thr
1 5 10 15

<210> 12

<211> 20

<212> PRT

<213> Conus marmoreus

<220>

<221> PEPTIDE

<222> (14)..(17)

<223> Xaa at residue 14 and 17 is Glu or gamma-carboxy-Glu; Xaa at residue 16 is Lys, N-methyl-Lys, N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 12

Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser Arg Phe Xaa Ile Xaa

1	5	10	15
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Xaa Asn Asp Phe
20

<210> 13
 <211> 10
 <212> PRT
 <213> Conus marmoreus

<400> 13
 Asn Ala Cys Cys Ile Val Arg Gln Cys Cys
 1 5 10

<210> 14
 <211> 11
 <212> PRT
 <213> Conus marmoreus

<400> 14
 Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser
 1 5 10

<210> 15
 <211> 11
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (3)
 <223> Xaa at residue 3 is Pro or hydroxy-Pro.

<400> 15
 Cys Cys Xaa Arg Arg Leu Ala Cys Cys Ile Ile
 1 5 10

<210> 16
 <211> 10
 <212> PRT
 <213> Conus characteristicus

<220>
 <221> PEPTIDE
 <222> (3)..(6)
 <223> Xaa at residue 3 and 6 is Pro or hydroxy-Pro; Xaa
 at residue 5 is Lys, N-methyl-Lys,
 N,N-dimethyl-Lys or N,N,N-trimethyl-Lys.

<400> 16
 Cys Cys Xaa Asn Xaa Xaa Cys Cys Phe Ile
 1 5 10

<210> 17
 <211> 10
 <212> PRT
 <213> Conus quercinus

<400> 17

Gly Cys Cys Ala Met Leu Thr Cys Cys Val
 1 5 10

<210> 18
 <211> 13
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> PEPTIDE
 <222> (6)..(13)
 <223> Xaa at residue 6 and 11 is Glu or
 gamma-carboxy-Glu; Xaa at residues 8, 12, and 13 is
 Trp (D or L), neo-Trp or halo-Trp (D or L).

<400> 18
 Leu Cys Cys Val Thr Xaa Asp Xaa Cys Cys Xaa Xaa Xaa
 1 5 10

<210> 19
 <211> 11
 <212> PRT
 <213> Conus gloriamaris

<220>
 <221> PEPTIDE
 <222> (5)
 <223> Xaa at residue 5 is Pro or hydroxy-Pro.

<400> 19
 Val Cys Cys Arg Xaa Val Gln Asp Cys Cys Ser
 1 5 10

<210> 20
 <211> 554
 <212> DNA
 <213> Conus textile

<220>
 <221> CDS
 <222> (65)..(250)

<400> 20
 ggtactcaac gaacttcaag acacattctt ttcacctgga cacgggaagc tgactacaag 60
 caga atg tgc tgt ctc cca gtg ttc gtc att ctt ctg ctg ctg att gca 109
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala 15
 1 5 10 15
 tct gca cct agc gtt gat gcc caa ccg aag acc aaa gat gat gtg ccc 157
 Ser Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro 30
 20 25 30
 ctg gca cct ttg cac gat aat gca aag agt gca cta caa cat ttg aac 205
 Leu Ala Pro Leu His Asp Asn Ala Lys Ser Ala Leu Gln His Leu Asn 45
 35 40 45
 caa cgc tgc tgc caa aca ttc tat tgg tgc tgt gtt caa ggg aaa 250
 Gln Arg Cys Cys Gln Thr Phe Tyr Trp Cys Cys Val Gln Gly Lys 60
 50 55 60

tgaatttggga tgagaccctt gogaactgtc catggatgtg agatttggaa agcagactgt 310
 tcctttcgca cgtgttcgtg gaattttgaa tggtcgttaa caacacgctg ccacttgcaa 370
 gctactatct ctctgtcctt tcatctgtgg aactggatga cctaacaact gaaatatcat 430
 agaaattttt cagtgggtat acactatgac catgtagtca gtaattacat catttggacc 490
 ttttgaaata tttttcaaaa tgttaagatt tttccccng gaaaggnctt ttgaagtaaa 550
 tatt 554

<210> 21
 <211> 62
 <212> PRT
 <213> Conus textile

<400> 21
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30
 Ala Pro Leu His Asp Asn Ala Lys Ser Ala Leu Gln His Leu Asn Gln
 35 40 45
 Arg Cys Cys Gln Thr Phe Tyr Trp Cys Cys Val Gln Gly Lys
 50 55 60

<210> 22
 <211> 416
 <212> DNA
 <213> Conus geographus

<220>
 <221> CDS
 <222> (1)..(183)

<400> 22
 atg tgc tgt ctc cca gtc ttc gtc att ctt ctg ttg ctg att aca tct 48
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Thr Ser
 1 5 10 15
 gca cct agc gtt gat gct cta ccg aag acc agg gat gat gtg ccc cta 96
 Ala Pro Ser Val Asp Ala Leu Pro Lys Thr Arg Asp Asp Val Pro Leu
 20 25 30
 gca tct ttc cac ggt gga tat aat gca agg aga atc cta caa agg cgt 144
 Ala Ser Phe His Gly Gly Tyr Asn Ala Arg Arg Ile Leu Gln Arg Arg
 35 40 45
 cag ggc tgg tgc tgc aaa gaa aat att gcg tgc tgt ata tagtggtaac 193
 Gln Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Ile
 50 55 60
 gggaaatgac tttggatgag acccctgcaa actgtccctg gatgtgaaat ttggaaagta 253
 gactgttcct ttgcgcgctg ttcgtggaat ttcaaattggt cgtcaacaac aactgctac 313
 ttgcaaagct actatctctc tgtcctttca tctgtggaac tgggtgatct aacagctgaa 373

atgtcgcaga aatttttcaa ttggtctata ctatgaccat gta

416

<210> 23
 <211> 61
 <212> PRT
 <213> Conus geographus

<400> 23
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Thr Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala Leu Pro Lys Thr Arg Asp Asp Val Pro Leu
 20 25 30
 Ala Ser Phe His Gly Gly Tyr Asn Ala Arg Arg Ile Leu Gln Arg Arg
 35 40 45
 Gln Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Ile
 50 55 60

<210> 24
 <211> 413
 <212> DNA
 <213> Conus quercinus

<220>
 <221> CDS
 <222> (1)..(186)

<400> 24
 atg cgc tgt gtc cca gtc ttc atc att ctt ctg ctg ctg agt cca tct 48
 Met Arg Cys Val Pro Val Phe Ile Ile Leu Leu Leu Leu Ser Pro Ser
 1 5 10 15
 gca cct agc gtt gat gcc cat ccg atg acc aaa gat gat gtg ccc cag 96
 Ala Pro Ser Val Asp Ala His Pro Met Thr Lys Asp Asp Val Pro Gln
 20 25 30
 gca tca ttc cat gat gat gca aag cga acc cta caa gta cct tgg atg 144
 Ala Ser Phe His Asp Asp Ala Lys Arg Thr Leu Gln Val Pro Trp Met
 35 40 45
 aaa cgc ggg tgc tgc gca agg ttg act tgc tgc gtt gga cga 186
 Lys Arg Gly Cys Cys Ala Arg Leu Thr Cys Cys Val Gly Arg
 50 55 60
 taaagggaaa tgactttgga tgagaccct gcgaactgtc cctggatgtg aaatttggac 246
 agcagactgc tcctttcgca cgtgttcgtg gaattttgaa tggtcgttaa caacacgtg 306
 ccacttgcaa gctattatct ctctgtccct ttatctgtgg aactggataa tctaacaact 366
 gaaatgtcat tgaaaatttt caatggatat atattatgat ccatata 413

<210> 25
 <211> 62
 <212> PRT
 <213> Conus quercinus

<400> 25
 Met Arg Cys Val Pro Val Phe Ile Ile Leu Leu Leu Leu Ser Pro Ser

1					5					10					15				
Ala	Pro	Ser	Val	Asp	Ala	His	Pro	Met	Thr	Lys	Asp	Asp	Val	Pro	Gln				
			20					25					30						
Ala	Ser	Phe	His	Asp	Asp	Ala	Lys	Arg	Thr	Leu	Gln	Val	Pro	Trp	Met				
		35					40					45							
Lys	Arg	Gly	Cys	Cys	Ala	Arg	Leu	Thr	Cys	Cys	Val	Gly	Arg						
	50					55					60								

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<210> 26
<211> 435
<212> DNA
<213> Conus imperialis
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<220>
<221> CDS
<222> (26) .. (211)
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<400> 26
aattcggaag ctgactacaa gcaga atg tac tgt ctc cca gtc ttc atc att      52
                               Met Tyr Cys Leu Pro Val Phe Ile Ile
                               1           5

ctt ctg ctg ctg att tca tct gca cct agc act cct ccc caa cca agg      100
Leu Leu Leu Leu Ile Ser Ser Ala Pro Ser Thr Pro Pro Gln Pro Arg
 10          15              20          25

aac aaa gat cgt gtg cac ctg ata tct tta ctc gat aat cac aag caa      148
Asn Lys Asp Arg Val His Leu Ile Ser Leu Leu Asp Asn His Lys Gln
                30          35          40

atc cta caa aga gat tgg aac agt tgc tgt ggg aaa aat cct ggt tgc      196
Ile Leu Gln Arg Asp Trp Asn Ser Cys Cys Gly Lys Asn Pro Gly Cys
            45              50          55

tgt cct tgg gga aaa tgactttgga tgagaccct gccaaactgtc cctggatgtg      251
Cys Pro Trp Gly Lys
        60

agatttggaag agcagaccgt ttgtggaatt ttgaatggc gttaacaaca cgctgccact      311

tgcaagctac aatctctctg tcctttcatc tttggaactg gatgatcaaa caactgaaat      371

gtcatagaaa tttttcaatg ggtatacaat atgtgggcat ttagtcagta attaccatcat      431

ttgg                                              435
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<210> 27 .
<211> 62
<212> PRT
<213> Conus imperialis
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<400> 27
Met Tyr Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ser Ser
1 5 10 15
Ala Pro Ser Thr Pro Pro Gln Pro Arg Asn Lys Asp Arg Val His Leu
20 25 30
Ile Ser Leu Leu Asp Asn His Lys Gln Ile Leu Gln Arg Asp Trp Asn

35 40 45
 Ser Cys Cys Gly Lys Asn Pro Gly Cys Cys Pro Trp Gly Lys
 50 55 60

<210> 28
 <211> 421
 <212> DNA
 <213> Conus geographus

<220>
 <221> CDS
 <222> (1)..(183)

<400> 28
 atg tgc tgt ctc cca gtc ttc gtc att ctt ctg ttg ctg att aca tct 48
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Thr Ser
 1 5 10 15
 gca cct agc gtt gat gct cta ccg aag acc agg gat gat gtg ccc cta 96
 Ala Pro Ser Val Asp Ala Leu Pro Lys Thr Arg Asp Asp Val Pro Leu
 20 25 30
 gca tct ttc cac ggt gga tat aat gca agg aga atc cta caa agg cgt 144
 Ala Ser Phe His Gly Gly Tyr Asn Ala Arg Arg Ile Leu Gln Arg Arg
 35 40 45
 cag ggc tgg tgc tgc aaa gaa aat att gcg tgc tgt gta tagtggtaac 193
 Gln Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Val
 50 55 60
 gggaaatgac tttggatgag acccctgcaa actgtccctg gatgtgaaat ttggaaagta 253
 gactgttcct ttcgcgcgtg ttcgtggaat ttcaaattggt cgtcaacaac aactgctac 313
 ttgcaaagct actatctctc tgtcctttca tctgtggaac tgggtgatct aacagctgaa 373
 atgtcgcaga aatttttcaa ttggtctata ctatgaccat gtagtcag 421

<210> 29
 <211> 61
 <212> PRT
 <213> Conus geographus

<400> 29
 Met Cys Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Thr Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala Leu Pro Lys Thr Arg Asp Asp Val Pro Leu
 20 25 30
 Ala Ser Phe His Gly Gly Tyr Asn Ala Arg Arg Ile Leu Gln Arg Arg
 35 40 45
 Gln Gly Trp Cys Cys Lys Glu Asn Ile Ala Cys Cys Val
 50 55 60

<210> 30
 <211> 431
 <212> DNA
 <213> Conus textile

<220>

<221> CDS

<222> (1)..(201)

<400> 30

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atg cgc tgt ttc cca gtc ttc atc att ctt ctg ctg cta att gca tct 48
Met Arg Cys Phe Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
  1              5              10              15

gca cct tgc ttt gat gcc cga acg aag acc gat gat gat gtg ccc ctg 96
Ala Pro Cys Phe Asp Ala Arg Thr Lys Thr Asp Asp Asp Val Pro Leu
              20              25              30

tca tct ctc cgc gat aat cta aag cga acg ata cga aca cgc ctg aac 144
Ser Ser Leu Arg Asp Asn Leu Lys Arg Thr Ile Arg Thr Arg Leu Asn
              35              40              45

ata cgc gag tgc tgc gag gat gga tgg tgc tgt act gct gca ccc tta 192
Ile Arg Glu Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu
              50              55              60

aca ggt cgt tagggataaaa ggaaaatggc tttggatgag acccctgcga 241
Thr Gly Arg
  65

attgtccctg gatgtgagat ttggaaagca gactgttcct ttcgcacgtg ttcgtggaat 301

ttcgaatggg cgtaacaac acgctgccac ttgcaagcca ccattctctt gtcctttcgt 361

atgtggaact gtatgatcta acaactgaaa tgtcagaaaag ttttcagtgg gtatacacta 421

tgatcgtata 431

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<210> 31

<211> 67

<212> PRT

<213> Conus textile

<400> 31

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Met Arg Cys Phe Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
  1              5              10              15

Ala Pro Cys Phe Asp Ala Arg Thr Lys Thr Asp Asp Asp Val Pro Leu
              20              25              30

Ser Ser Leu Arg Asp Asn Leu Lys Arg Thr Ile Arg Thr Arg Leu Asn
              35              40              45

Ile Arg Glu Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu
              50              55              60

Thr Gly Arg
  65

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<210> 32

<211> 441

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (1)..(201)

<400> 32
 atg cgc tgt ttc cca gtc ttc atc att ctt ctg ttg cta att gca tct 48
 Met Arg Cys Phe Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15

gca cct tgc ttt gat gcc cga acg aag acc gat gat gat gtg ccc ctg 96
 Ala Pro Cys Phe Asp Ala Arg Thr Lys Thr Asp Asp Asp Val Pro Leu
 20 25 30

tca tct ctc cgc gat aat cta aag cga acg ata cga aca cgc ctg aac 144
 Ser Ser Leu Arg Asp Asn Leu Lys Arg Thr Ile Arg Thr Arg Leu Asn
 35 40 45

ata cgc ggg tgc tgc gag gat gga tgg tgc tgt act gct gca ccc tta 192
 Ile Arg Gly Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu
 50 55 60

aca ggt cgt tagggataaa ggaaaatggc tttggatgag acccctgcaa 241
 Thr Gly Arg
 65

attgtccctg gatgtgagat ttggaaagca gactgttcct ttgcacgtg ttcgtggaat 301
 ttgcaatggt cgtaacaac acgctgccac ttgcaagcca ccatctctct gtcctttcgt 361
 atgtggaact gtatgatcta acaactgaaa tgtcagaaag ttttcagtgg gtatacacta 421
 tgatcgtata gtcagtaatt 441

<210> 33
 <211> 67
 <212> PRT
 <213> Conus textile

<400> 33
 Met Arg Cys Phe Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15

Ala Pro Cys Phe Asp Ala Arg Thr Lys Thr Asp Asp Asp Val Pro Leu
 20 25 30

Ser Ser Leu Arg Asp Asn Leu Lys Arg Thr Ile Arg Thr Arg Leu Asn
 35 40 45

Ile Arg Gly Cys Cys Glu Asp Gly Trp Cys Cys Thr Ala Ala Pro Leu
 50 55 60

Thr Gly Arg
 65

<210> 34
 <211> 416
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (1)..(210)

<400> 34
 atg cgc tgc ctc cca gtc ttc gtc att ctt ctg ctg ctg att gca tct 48
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala Ser

1 5 10 15

gca cct agc gtt gat gcc cga ccg aag acc aaa gat gat atg ccc ctg 96
 Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30

gca tct ttc cat gat aat gca aag cga atc ctg caa ata ctt cag gac 144
 Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln Asp
 35 40 45

aga aat ggt tgc tgc aga gca gga gac tgc tgt tca cga ttt gag ata 192
 Arg Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser Arg Phe Glu Ile
 50 55 60

aag gaa aat gac ttt gga tgagaccct gcaaactgtc cttggatgtg 240
 Lys Glu Asn Asp Phe Gly
 65 70

agatttggaa agcagactgt tcctttcgca cgtgttcgtg gaatttcgaa tggtcgttaa 300

caacacgctg ccacttgcaa gctactatct ctctgtcctt ttgtctgtgg aactgtatga 360

tcaaacaact gaaatgtcat agaaattttt cagtgggtaa acactatgac catgta 416

<210> 35
 <211> 70
 <212> PRT
 <213> Conus marmoreus

<400> 35
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15

Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30

Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln Asp
 35 40 45

Arg Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser Arg Phe Glu Ile
 50 55 60

Lys Glu Asn Asp Phe Gly
 65 70

<210> 36
 <211> 487
 <212> DNA
 <213> Conus marmoreus

<220>
 <221> CDS
 <222> (3)..(179)

<400> 36

ga atg cgc tgc ctc cca gtc ttc gtc att ctt ctg ctg ctg att gca 47
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala
 1 5 10 15

tct gca cct agc gtt gat gcc cga ccg aag acc aaa gat gat atg ccc 95
 Ser Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro
 20 25 30

ctg gca tct ttc cac gat aat gca aag cga atc ctg caa ata ctt cag 143
Leu Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln
35 40 45

gac aga aat gct tgc tgc ata gta agg cag tgc tgt tgatgatttg 189
Asp Arg Asn Ala Cys Cys Ile Val Arg Gln Cys Cys
50 55

agataaaagga aaatgacttt ggatgagacc cctgcaaact gtccctggat gtgagatttg 249
gaaagcagac tgttcctttc gcacgtgttc gtggaatttc gaatggtcgt taacaacacg 309
ctgccacttg caagctacta tctctctgtc ctttcatctg tggaactgta tgatcaaaca 369
actgaaatgt catagaaatt tttcagtggg taaacactat gatcatgtag tcagtaatta 429
catcattttg aattccatca agcttatcga taccgtcgac ctcgaggggg gqcccqgt 487

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<210> 37
<211> 59
<212> PRT
<213> Conus marmoreus
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<400> 37
Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala Ser
 1             5             10             15
Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro Leu
 20             25             30
Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln Asp
 35             40             45
Arg Asn Ala Cys Cys Ile Val Arg Gln Cys Cys
 50             55

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<210> 38
<211> 370
<212> DNA
<213> Conus marmoreus
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<220>  
<221> CDS  
<222> (1)..(180)
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<400> 38																
atg	cgc	tgc	ctc	cca	gtc	ttt	gtc	att	ctt	ctg	ctg	ctg	att	gca	tct	48
Met	Arg	Cys	Leu	Pro	Val	Phe	Val	Ile	Leu	Leu	Leu	Leu	Ile	Ala	Ser	
1				5					10					15		
gca cct agc gtt gat gcc cga ccg aag acc aaa gat gat atg ccc ctg																96
Ala	Pro	Ser	Val	Asp	Ala	Arg	Pro	Lys	Thr	Lys	Asp	Asp	Met	Pro	Leu	
			20					25					30			
gca tct ttc cat gat aat gca aag cga atc ctg caa ata ctt cag gac																144
Ala	Ser	Phe	His	Asp	Asn	Ala	Lys	Arg	Ile	Leu	Gln	Ile	Leu	Gln	Asp	
		35					40					45				
aga aat ggt tgc tgc aga gca gga gac tgc tgt tca tgatttgaga																190
Arg	Asn	Gly	Cys	Cys	Arg	Ala	Gly	Asp	Cys	Cys	Ser					
	50					55					60					

taaagggaaa tgactttgga tgagaccctt gcaaactgtc cttggatgtg agatttggaa 250
 agcagactgt tcctttcgca cgtgttcgtg gaatttcgaa tggtcgttaa caacacgtg 310
 ccacttgcaa gctactatct ctctgtcctt tcctctgtgg aactgtatga tcaaacaact 370

<210> 39
 <211> 60
 <212> PRT
 <213> *Conus marmoreus*

<400> 39
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Ile Ala Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala Arg Pro Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30
 Ala Ser Phe His Asp Asn Ala Lys Arg Ile Leu Gln Ile Leu Gln Asp
 35 40 45
 Arg Asn Gly Cys Cys Arg Ala Gly Asp Cys Cys Ser
 50 55 60

<210> 40
 <211> 413
 <212> DNA
 <213> *Conus characteristicus*

<220>
 <221> CDS
 <222> (1)..(192)

<400> 40
 atg cgc tgt ctc ccg gtc ttc atc att ctt ctg ctg ctg att gca tct 48
 Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Ile Ala Ser
 1 5 10 15
 gca cct ggc gtt gat gcc caa ccg aag acc aaa tat aat gcg ccc ctg 96
 Ala Pro Gly Val Asp Ala Gln Pro Lys Thr Lys Tyr Asn Ala Pro Leu
 20 25 30
 aca tct ctc cac gat aat gca aag ggt ata cta caa gaa cat tgg aac 144
 Thr Ser Leu His Asp Asn Ala Lys Gly Ile Leu Gln Glu His Trp Asn
 35 40 45
 aaa cgc tgc tgc ccc aga agg ctt gcc tgc tgt att ata gga cgg aaa 192
 Lys Arg Cys Cys Pro Arg Arg Leu Ala Cys Cys Ile Ile Gly Arg Lys
 50 55 60
 tgaatgattt tgggtgagat ccctgcaaac tgtccctgga tttgaatttt ggaaagcaga 252
 ctgttccttt cgcacgtgtt cgtggaattt cgaatgggtc ttaacaacac gctgccactt 312
 gcaagctact atctctctgt cctttttctc tgtgaaactg gatgggtctaa caactgaaat 372
 gtcatagaaa attttcaatg ggtatactct atgaccatct a 413

<210> 41
 <211> 64
 <212> PRT

<213> Conus characteristicus

<400> 41

Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
1 5 10 15

Ala Pro Gly Val Asp Ala Gln Pro Lys Thr Lys Tyr Asn Ala Pro Leu
20 25 30

Thr Ser Leu His Asp Asn Ala Lys Gly Ile Leu Gln Glu His Trp Asn
35 40 45

Lys Arg Cys Cys Pro Arg Arg Leu Ala Cys Cys Ile Ile Gly Arg Lys
50 55 60

<210> 42

<211> 410

<212> DNA

<213> Conus characteristicus

<220>

<221> CDS

<222> (1)..(189)

<400> 42

atg cgc tgt ctc cca gtc ttc atc att ctt ctg ctg ctg att gca tct 48
Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
1 5 10 15

gca cct ggc gtt gat gcc caa ccg aag acc aaa tat gat gcg ccc ctg 96
Ala Pro Gly Val Asp Ala Gln Pro Lys Thr Lys Tyr Asp Ala Pro Leu
20 25 30

aca tct ctc cac gat aat gca aag ggt ata cta caa gaa cat tgg aac 144
Thr Ser Leu His Asp Asn Ala Lys Gly Ile Leu Gln Glu His Trp Asn
35 40 45

aaa cgc tgc tgc ccc aac aag cct tgc tgt ttt ata gga agg aaa 189
Lys Arg Cys Cys Pro Asn Lys Pro Cys Cys Phe Ile Gly Arg Lys
50 55 60

tgaatgattt tgggtgagac cctgcaaac tgtccctgga tttgaatttt ggaaagcaga 249

ctgttccttt cgcaagtgtt cgtggaattt cgaatggctcg ttaacaacac gctgccactt 309

gcaagctact atctctctgt cctttttctc tgtgaaactg gatgggtctaa caactgagat 369

gtcatagaaa attttcaatc ggtgtactct atgaccatct a 410

<210> 43

<211> 63

<212> PRT

<213> Conus characteristicus

<400> 43

Met Arg Cys Leu Pro Val Phe Ile Ile Leu Leu Leu Leu Ile Ala Ser
1 5 10 15

Ala Pro Gly Val Asp Ala Gln Pro Lys Thr Lys Tyr Asp Ala Pro Leu
20 25 30

Thr Ser Leu His Asp Asn Ala Lys Gly Ile Leu Gln Glu His Trp Asn

35 40 45
 Lys Arg Cys Cys Pro Asn Lys Pro Cys Cys Phe Ile Gly Arg Lys
 50 55 60

<210> 44
 <211> 413
 <212> DNA
 <213> Conus quercinus

<220>
 <221> CDS
 <222> (1)..(186)

<400> 44
 atg cgc tgt gtc cca gtc ttc atc att ctt ctg ctg ctg agt cca tct 48
 Met Arg Cys Val Pro Val Phe Ile Ile Leu Leu Leu Leu Ser Pro Ser
 1 5 10 15
 gca cct agc gtt gat gcc cat ccg atg acc aaa gat gat gta ccc cag 96
 Ala Pro Ser Val Asp Ala His Pro Met Thr Lys Asp Asp Val Pro Gln
 20 25 30
 gca tct ctc cat gat gat gca aag cga acc cta caa gta cct tgg atg 144
 Ala Ser Leu His Asp Asp Ala Lys Arg Thr Leu Gln Val Pro Trp Met
 35 40 45
 aaa cgc ggg tgc tgc gca atg ttg act tgc tgc gtt gga cga 186
 Lys Arg Gly Cys Cys Ala Met Leu Thr Cys Cys Val Gly Arg
 50 55 60
 taaagggaaa tgacttttga tgagacccct acgaactgtc cctggatgtg aaatttggac 246
 agcagactgc tcctttcgca cgtgttcgtg gaatttcgaa tggtcgttaa caacacgtg 306
 ccacttgcaa gctattatct ctctgtccct ttatctgtgg aactggataa tctaacaact 366
 gaaacgtcat tgaaaatttt caatggatat atattatgat ccatata 413

<210> 45
 <211> 62
 <212> PRT
 <213> Conus quercinus

<400> 45
 Met Arg Cys Val Pro Val Phe Ile Ile Leu Leu Leu Leu Ser Pro Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala His Pro Met Thr Lys Asp Asp Val Pro Gln
 20 25 30
 Ala Ser Leu His Asp Asp Ala Lys Arg Thr Leu Gln Val Pro Trp Met
 35 40 45
 Lys Arg Gly Cys Cys Ala Met Leu Thr Cys Cys Val Gly Arg
 50 55 60

<210> 46
 <211> 735
 <212> DNA
 <213> Conus gloriamaris

<220>

<221> CDS

<222> (70)..(258)

<400> 46

gggcaggtac tcaacgaact tcaggacaca ttcttttcac ctggacacgg gaaactgact 60

ataagcaga atg cgc tac cta cca gtc ttc gtc att ctt ctg ctg ctg att 111
 Met Arg Tyr Leu Pro Val Phe Val Ile Leu Leu Leu Ile
 1 5 10

gca tct ata cct agc gat act gtc caa ctg aag acc aaa gat gat atg 159
 Ala Ser Ile Pro Ser Asp Thr Val Gln Leu Lys Thr Lys Asp Asp Met
 15 20 25 30

ccc ctg gca tct ttc cac ggt aat gga aga cga atc ctg cga atg ctt 207
 Pro Leu Ala Ser Phe His Gly Asn Gly Arg Arg Ile Leu Arg Met Leu
 35 40 45

tca aac aaa cgc tta tgc tgt gtc acc gag gat tgg tgc tgt gaa tgg 255
 Ser Asn Lys Arg Leu Cys Cys Val Thr Glu Asp Trp Cys Cys Glu Trp
 50 55 60

tgg taaaggaaaa tgactttgga tgagaccct gcaaactgtt tctggatgtg 308
 Trp

agatttggaa agcagactgt tctttcgcac gtattcgtga aatttcgaat ggtcgttaac 368

aacacgctgc cacttgcaag ctgctatctc tctgtctttt catctgtgga actgtatgat 428

ctaacaactg aaatgtcata gacatttttc attgggtata cactatgacc atgtagccag 488

taattacatc atttggacct tttggatatt tttcagtatg taagtgtgtt cccttaaaaa 548

gtcctttgta attatgtatt ttaanaattt angttttgca cataaattgt aaaacgctgt 608

cctttctgtt gntcctacat cantggtggg gaaaagnaaa atgtttggcc ntgggtcaaat 668

ttaaataatn accctgccgt ttnaatgcng ttattantgg tatttttnaac nttgnacggt 728

taaactt 735

<210> 47

<211> 63

<212> PRT

<213> Conus gloriamaris

<400> 47

Met Arg Tyr Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15

Ile Pro Ser Asp Thr Val Gln Leu Lys Thr Lys Asp Asp Met Pro Leu
 20 25 30

Ala Ser Phe His Gly Asn Gly Arg Arg Ile Leu Arg Met Leu Ser Asn
 35 40 45

Lys Arg Leu Cys Cys Val Thr Glu Asp Trp Cys Cys Glu Trp Trp
 50 55 60

<210> 48

<211> 374

<212> DNA
 <213> Conus gloriamaris

<220>
 <221> CDS
 <222> (3)..(188)

<400> 48
 ga atg cgc tgt ctc cca gtc ttc gtc att ctt ctg ctg ctg att gca 47
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala
 1 5 10 15
 tct gca cct agc gtt gat gcc caa ccg aag acc aaa gat gat gtg ccc 95
 Ser Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro
 20 25 30
 ctg gca cct ttg cac gat aat ata agg agt act cta caa aca ctt cgg 143
 Leu Ala Pro Leu His Asp Asn Ile Arg Ser Thr Leu Gln Thr Leu Arg
 35 40 45
 aag aaa gtc tgc tgc cgc cca gtg cag gat tgc tgt tca ggg aaa 188
 Lys Lys Val Cys Cys Arg Pro Val Gln Asp Cys Cys Ser Gly Lys
 50 55 60
 tgaagggaaa tgaatttgga tgagaccct gcgaactgtc cctggatgtg agatttgga 248
 agcagactgt tcctttcgca cgtgttcgtg gaatttcgaa tggtcgttaa caacacgtg 308
 ccacttgcaa gctactatct ctctgtcctt tcactctgagg aactggatga cctaaagctt 368
 gtgatc 374

<210> 49
 <211> 62
 <212> PRT
 <213> Conus gloriamaris

<400> 49
 Met Arg Cys Leu Pro Val Phe Val Ile Leu Leu Leu Leu Ile Ala Ser
 1 5 10 15
 Ala Pro Ser Val Asp Ala Gln Pro Lys Thr Lys Asp Asp Val Pro Leu
 20 25 30
 Ala Pro Leu His Asp Asn Ile Arg Ser Thr Leu Gln Thr Leu Arg Lys
 35 40 45
 Lys Val Cys Cys Arg Pro Val Gln Asp Cys Cys Ser Gly Lys
 50 55 60